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TO: Examiner Zeman
USPTO

Date: 10 December 1997

Fax No. (703) 305-7939

FROM: Ken Goldman

Number of Pages: 15
(Including cover page)

RE: _____

Message: Per our conversation, here are the allowed
claims in USN 08/040,564, 08/440,769 and
08/472,821.

Please contact Gyne Riser at (510) 923-3003 if you have any problems receiving this transmission.

Here are allowed claims 24, 26-29, 31-44 and 50-57 in U.S. Serial No. 08/040,564 (issue fee paid):

24. A purified preparation of an oligonucleotide, wherein the oligonucleotide is capable of selectively hybridizing to the genome of a hepatitis C virus (HCV), or its complement, relative to other viral agents, and further wherein the oligonucleotide comprises a contiguous sequence of at least 10 nucleotides fully complementary to either strand of the nucleotide residue sequence depicted in Figure 1.

26. The purified preparation of claim 24 wherein the oligonucleotide comprises a contiguous sequence of at least 12 nucleotides fully complementary to either strand of the nucleotide residue sequence depicted in Figure 1.

27. The purified preparation of claim 24 wherein the oligonucleotide comprises a contiguous sequence of at least 15 nucleotides fully complementary to either strand of the nucleotide residue sequence depicted in Figure 1.

28. The purified preparation of claim 24 wherein the oligonucleotide comprises a contiguous sequence of at least 20 nucleotides fully complementary to either strand of the nucleotide residue sequence depicted in Figure 1.

29. The purified preparation of claim 24 wherein the oligonucleotide is a primer for a DNA polymerase or a reverse transcriptase.

31. The purified preparation of claim 24 wherein the contiguous sequence is a conserved HCV nucleotide sequence.

32. The purified preparation of claim 31 wherein the conserved sequence is located in the sequence of nucleotide numbers from the 5' terminus to 200 in Figure 1.

33. The purified preparation of claim 31 wherein the conserved sequence is located in the sequence of nucleotide numbers from 4000 to 5000 in Figure 1.

34. The purified preparation of claim 31 wherein the conserved sequence is located in the sequence of nucleotide numbers from 8000 to 9040 in Figure 1.

35. The purified preparation of claim 31 wherein the conserved sequence is located in the sequence of nucleotide numbers from -318 to 174 in Figure 1.

36. The purified preparation of claim 31 wherein the conserved sequence is located in the sequence of nucleotide numbers from 4056 to 4448 in Figure 1.

37. The purified preparation of claim 31 wherein the conserved sequence is located in the sequence of nucleotide numbers from 4378 to 4902 in Figure 1.

38. The purified preparation of claim 31 wherein the conserved sequence is located in the sequence of nucleotide numbers from 4042 to 4059 in Figure 1.

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39. The purified preparation of claim 31 wherein the conserved sequence is located in the sequence of nucleotide numbers from 4456 to 4470 in Figure 1.

40. The purified preparation of claim 31 wherein the conserved sequence is located in the sequence of nucleotide numbers from 8209 to 8217 in Figure 1.

41. The purified preparation of claim 31, wherein the oligonucleotide hybridizes to the sequence of nucleotide numbers from -313 to -282 in Figure 1.

42. The purified preparation of claim 31, wherein the oligonucleotide hybridizes to the sequence of nucleotide numbers from -203 to -173 in Figure 1.

43. The purified preparation of claim 31, wherein the oligonucleotide hybridizes to the sequence of nucleotide numbers from -252 to -221 in Figure 1.

44. The purified preparation of claim 31, wherein the oligonucleotide hybridizes to a sequence located between nucleotide 16 and nucleotide 486 in Figure 1.

50. (New) The purified preparation of claim 24 wherein the oligonucleotide comprises a sequence selected from the group consisting of:

5' - TCC CTT GCT CGA TGT ACG GTA AGT GCT GAG AGC ACT CTT CCA
TCT CAT CGA ACT CTC GGT AGA GGA CTT CCC TGT CAG GT - 3',

5' - CTG TCA GGT ATG ATT GCC GGC TTC CCG GAC - 3',

5' - TTT GGC TAG TGG TTA GTG GGC TGG TGA CAG - 3',

5' - AAG CCA CCG TGT GCG CTA GGG CTC AAG CCC - 3',

5' - CAG GAT GCT GTC TCC CGC ACT CAA CGT - 3',

5' - AGT GCA GTG GAT GAA CCG GCT GAT AGC CTT - 3',

5' - TCC TGA GGC GAC TGC ACC AGT GGA TAA GCT - 3',

5' - CAG GAT GCT GTC TCC CGC ACT CAA CGT C - 3',

5' - ATC AGG ACC GGG GTG AGA ACA ATT ACC ACT - 3',

5' - AGA GAC AAC CAT GAG GTC CCC GGT GTT C - 3',

5' - TCG GAC CTT TAC CTG GTC ACG AGG CAC - 3',

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5' - ACC TTC CCC ATT AAT GCC TAC ACC ACG GGC - 3',
5' - TCC ATC TCT CAA GGC AAC TTG CAC CGC TAA - 3',
5' - TCC ATG GCT GTC CGC TTC CAC CTC CAA AGT - 3',
5' - GCG ACA ATA CGA CAA CAT CCT CTG AGC CCG - 3',
5' - AGC AGA CAA GGG GCC TCC TAG GGT GCA TAA T - 3',
5' - CAC CTA TGT TTA TAA CCA TCT CAC TCC TCT - 3',
5' - CTC TGT CAC CAT ATT ACA AGC GCT ATA TCA - 3',
5' - CTC GTT GCT ACG TCA CCA CAA TTT GGT GTA - 3',
5' - TGC TTG TGG ATG ATG CTA CTC ATA TCC CAA - 3',
5' - AGC AGC GGC GTC AAA AGT GAA GGC TAA CTT - 3',
5' - TTC TCG TAT GAT ACC CGC TGC TTT GAC TCC - 3',
5' - TGT GTG GCG ACG ACT TAG TCG TTA TCT GTG - 3',
5' - CAC ACT CCA GTC AAT TCC TGG CTA GGC AAC - 3',
5' - CTG GCT TGA AGA ATC - 3',
5' - AGT TAG GCT GGT GAT TAT GC - 3',
5' - GAA CGT TGC GAT CTG GAA GAC AGG GAC AGG - 3',
5' - TAT CAG TTA TGC CAA CGG AAG CGG CCC CGA - 3',
5' - CTG GTT AGC AGG GCT TTT CTA TCA CCA CAA - 3',
5' - AAG GTC CTG GTA GTG CTG CTG CTA TTT GCC - 3',
5' - ACT GGA CGA CGC AAG GTT GCA ATT GCT CTA - 3',
5' - TTC GAC GTC ACA TCG ATC TGC TTG TCG GGA - 3',
5' - GGT GAC GTG GGT TTC - 3',
5' - GGC TTT ACC ACG TCA CCA ATG ATT GCC CTA - 3',

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5' - TTT GGG TAA GGT CAT CGA TAC CCT TAC GTG - 3',
5' - GAA GCC GCA CGT AAG - 3',
5' - CCG GCG TAG GTC GCG CAA TTT GGG TAA - 3',
5' - TCA GAT CGT TGG TGG AGT TTA CTT GTT GCC - 3',
5' - CCA TAG TGG TCT GCG GAA CCG GTG AGT ACA - 3',
5' - ATT GCG AGA TCT ACG GGG CCT GCT ACT CCA - 3',
5' - ATA GCG GCC GCC CTC GAT TGC GAG AGC TAC - 3',
5' - AAT TCG GGC GGC CGC CAT ACG A - 3',
5' - CTT GAT CTA CCT CCA ATC ATT CAA AGA CTC - 3',
5' - TCT TCA ACT GGG CAG TAA GAA CAA AGC TCA - 3',
5' - AAT TCG CGG CCG CCA TAC GAT TTA GGT GAC ACT ATA GAA T15-3',
5' - TTC GCG GCC GCT ACA GCG GGG GAG ACA T - 3',
5' - AAT TCG CGG CCG CCA TAC GA - 3',
5' - CGA TGA AGG TTG GGG TAA ACA CTC CGG CCT - 3',
5' - GAT CCT GGA ATT CTG ATA AGA CCT TAA GAC TAT TTT AA - 3',
5' - AAT TTG GGA ATT CCA TAA TGA GAC CCT TAA GGT ATT ACT CAG CT
- 3',
5' - GAG TGC TCA AGC TTC AAA ACA AAA TGG CTC ACT TTC TAT CCC
AGA CAA AGC AGA GT - 3',
5' - GAG TGC TCG ACT CAT TAG GGG GAA ACA TGG TTC CCC CGG GAG
GCG AA - 3',
5' - GAG TGC TCA AGC TTC AAA ACA AAA TGG GGC TCT ACC ACG TCA
CCA ATG ATT GCC CTA AC - 3',
5' - GAG TGC TCG TCG ACT CAT TAA GGG GAC CAG TTC ATC ATC ATA
TCC CAT GCC AT - 3',

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5' - GAG TGC AGC TTC AAA ACA AAA TGA GCA CGA ATC CTA AAC CTC
AAA AAA AAA AC- 3',

5' - GAG TGC TCG TCG ACT CAT TAA CCC AAA TTG CGC GAC CTA CGC
CGG GGG TCT GT - 3',

5' - GAG TGC TCA AGC TTA CAA AAC AAA ATG GCA CCA GGC GCC AAG
CAG AAC GTC CAG CTG ATC - 3',

5' - GAG TGC TCC TCG AGG TCG ACT CAT TAC TCG GAC CTG TCC CTA
TCT TCC AGA TCG CAA CG - 3',

5' - GGA TCC GCT AGC GGC GCC AAG CAG AAC GTC CAG CTG ATC AAC
ACC - 3',

5' - GGA TCC AAG CTT TTA CTC GGA CCT GTC CCT ATC TTC CAG ATC
GCA ACG - 3',

5' - CAA TCA TAC CTG ACA G - 3',

5' - GAT AAC CTC TGC CTG A - 3',

5' - GCA TGT CAT GAT GTA T - 3',

5' - ACA ATA CTG GTG TCA C - 3',

5' - CCA GCG GTG GCC TGG TAT TG - 3',

5' - TTT GGG TAA GGT CAT CGA TAC CCT TAC GTG - 3',

5' - ATA TGC GGC CGC CTT CCG TTG GAC TAA - 3',

5' - AAT TCG CGG CCG CCA TAC GAT TTA GGT GAC ACT ATA GAA CCC
CCC CCC CCC CCC - 3',

5' - CGA CAA GAA AGA CAG A - 3',

5' - CGT TGG CAT AAC TGA T - 3',

5' - CTC TAT GGC AAT GAG G - 3',

5' - AGC TTC GAC GTC ACA T - 3',

5' - CTT GAA TTC GCA ATT TGG GTA AGG TCA TCG ATA CCC TTA CG-3',

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5' - CTT GAA TTC GAT AGA GCA ATT GCA ACC TTG CGT CGT CC - 3',

5' - CTT GAA TTC GGA CGA CGC AAG GTT GCA ATT GCT CTA TC - 3',

5' - CTT GAA TTC CAG CCG GTG TTG AGG CTA TCA TTG CAG TTC - 3',

5' - TGA ACT ATG CAA CAG G - 3',

5' - GGA GTG TGC AGG ATG G - 3',

5' - AAG GTT GCA ATT GCT C - 3',

5' - ACT AAC AGG ACC TTC G - 3',

5' - TAA CGG GTC ACC GCA T - 3',

5' - GTA ATA TGG TGA CAG AGT CA - 3',

5' - GAT CTC TAG AGA AAT CAA TAT GGT GAC AGA GTC A - 3', and

5' - CCC AGC GGC GTA CGC GCT GGA CAC GGA GGT GGC CGC GTC GTG
TGG CGG TGT TGT TCT CGT CGG GTT GAT GGC GC - 3'.

51. The purified preparation of claim 24 wherein the oligonucleotide comprises a contiguous sequence of at least 10 nucleotides fully complementary to a unique nucleotide residue sequence in either strand of the nucleotide residue sequence depicted in Figure 1.

52. The purified preparation of claim 24 wherein the oligonucleotide comprises a contiguous sequence of at least 12 nucleotides fully complementary to a unique nucleotide residue sequence in either strand of the nucleotide residue sequence depicted in Figure 1.

53. The purified preparation of claim 24 wherein the oligonucleotide comprises a contiguous sequence of at least 15 nucleotides fully complementary to a unique nucleotide residue sequence in either strand of the nucleotide residue sequence depicted in Figure 1.

54. The purified preparation of claim 24 wherein the oligonucleotide comprises a contiguous sequence of at least 20 nucleotides fully complementary to a unique nucleotide residue sequence in either strand of the nucleotide residue sequence depicted in Figure 1.

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55. The purified preparation of claim 26 wherein the oligonucleotide is a primer for a DNA polymerase or a reverse transcriptase.

56. The purified preparation of claim 51 wherein the oligonucleotide is a primer for a DNA polymerase or a reverse transcriptase.

57. The purified preparation of claim 52 wherein the oligonucleotide is a primer for a DNA polymerase or a reverse transcriptase.

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Here are allowed claims 29-41 in U.S. Serial No. 08/440,769 (issue fee paid):

29. A method for detecting an HCV sequence in a test sample suspected of containing an HCV polynucleotide, wherein the HCV polynucleotide comprises a selected target region, said method comprising:

(a) providing an oligonucleotide capable of selectively hybridizing to the genome of a hepatitis C virus (HCV), or its complement, wherein the oligonucleotide comprises a contiguous sequence of at least 8 nucleotides fully complementary to the genome of an HCV or its complement;

(b) providing a set of primer oligonucleotides which are primers for the polymerase chain reaction method and which flank the target region;

(c) amplifying the target region via a polymerase chain reaction method to obtain an amplified test sample;

(d) incubating the amplified test sample with the oligonucleotide of step (a) under conditions which allow hybrid duplexes to form between the oligonucleotide and the target region specifically relative to other viral agents; and

(e) detecting any hybrids formed between the target region and the oligonucleotide, wherein the presence of said hybrid duplex is indicative of HCV being present in the test sample.

30. The method of claim 29 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 10 nucleotides fully complementary to the genome of an HCV or its complement.

31. The method of claim 29 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 12 nucleotides fully complementary to the genome of an HCV or its complement.

32. The method of claim 29 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 15 nucleotides fully complementary to the genome of an HCV or its complement.

33. The method of claim 29 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 20 nucleotides fully complementary to the genome of an HCV or its complement.

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34. The method of claim 29 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 10 nucleotides fully complementary to a nucleotide residue sequence present in one of the strands of Figure 1.

35. The method of claim 29 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 10 nucleotides fully complementary to a unique nucleotide residue sequence of the genome of an HCV or its complement.

36. The method of claim 29 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 12 nucleotides fully complementary to a unique nucleotide residue sequence of the genome of an HCV or its complement.

37. The method of claim 29 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 15 nucleotides fully complementary to a unique nucleotide residue sequence of the genome of an HCV or its complement.

38. The method of claim 29 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 20 nucleotides fully complementary to a unique nucleotide residue sequence of the genome of an HCV or its complement.

39. The method of claim 29 wherein the oligonucleotide of step (a) comprises a contiguous sequence of at least 10 nucleotides fully complementary to a unique nucleotide residue sequence present in one of the strands of Figure 1.

40. The method of claim 29 wherein the contiguous sequence is a conserved HCV nucleotide sequence.

41. The method of claim 29 wherein the oligonucleotide provided in step (a) comprises a sequence selected from the group consisting of:

5' - TCC CTT GCT CGA TGT ACG GTA AGT GCT GAG AGC ACT CTT CCA
TCT CAT CGA ACT CTC GGT AGA GGA CTT CCC TGT CAG GT - 3',

5' - CTG TCA GGT ATG ATT GCC GGC TTC CCG GAC - 3',

5' - TTT GGC TAG TGG TTA GTG GGC TGG TGA CAG - 3',

5' - AAG CCA CCG TGT GCG CTA GGG CTC AAG CCC - 3',

5' - CAG GAT GCT GTC TCC CGC ACT CAA CGT - 3',

5' - AGT GCA GTG GAT GAA CCG GCT GAT AGC CTT - 3',

5' - TCC TGA GGC GAC TGC ACC AGT GGA TAA GCT - 3',

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5' - CAG GAT GCT GTC TCC CGC ACT CAA CGT C - 3',
5' - ATC AGG ACC GGG GTG AGA ACA ATT ACC ACT - 3',
5' - AGA GAC AAC CAT GAG GTC CCC GGT GTT C - 3',
5' - TCG GAC CTT TAC CTG GTC ACG AGG CAC - 3',
5' - ACC TTC CCC ATT AAT GCC TAC ACC ACG GGC - 3',
5' - TCC ATC TCT CAA GGC AAC TTG CAC CGC TAA - 3',
5' - TCC ATG GCT GTC CGC TTC CAC CTC CAA AGT - 3',
5' - GCG ACA ATA CGA CAA CAT CCT CTG AGC CCG - 3',
5' - AGC AGA CAA GGG GCC TCC TAG GGT GCA TAA T - 3',
5' - CAC CTA TGT TTA TAA CCA TCT CAC TCC TCT - 3',
5' - CTC TGT CAC CAT ATT ACA AGC GCT ATA TCA - 3',
5' - CTC GTT GCT ACG TCA CCA CAA TTT GGT GTA - 3',
5' - TGC TTG TGG ATG ATG CTA CTC ATA TCC CAA - 3',
5' - AGC AGC GGC GTC AAA AGT GAA GGC TAA CTT - 3',
5' - TTC TCG TAT GAT ACC CGC TGC TTT GAC TCC - 3',
5' - TGT GTG GCG ACG ACT TAG TCG TTA TCT GTG - 3',
5' - CAC ACT CCA GTC AAT TCC TGG CTA GGC AAC - 3',
5' - CTG GCT TGA AGA ATC - 3',
5' - AGT TAG GCT GGT GAT TAT GC - 3',
5' - GAA CGT TGC GAT CTG GAA GAC AGG GAC AGG - 3',
5' - TAT CAG TTA TGC CAA CGG AAG CGG CCC CGA - 3',
5' - CTG GTT AGC AGG GCT TTT CTA TCA CCA CAA - 3',
5' - AAG GTC CTG GTA GTG CTG CTG CTA TTT GCC - 3',

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5' - ACT GGA CGA CGC AAG GTT GCA ATT GCT CTA - 3',
5' - TTC GAC GTC ACA TCG ATC TGC TTG TCG GGA - 3',
5' - GGT GAC GTG GGT TTC - 3',
5' - GGC TTT ACC ACG TCA CCA ATG ATT GCC CTA - 3',
5' - TTT GGG TAA GGT CAT CGA TAC CCT TAC GTG - 3',
5' - GAA GCC GCA CGT AAG - 3',
5' - CCG GCG TAG GTC GCG CAA TTT GGG TAA - 3',
5' - TCA GAT CGT TGG TGG AGT TTA CTT GTT GCC - 3',
5' - CCA TAG TGG TCT GCG GAA CCG GTG AGT ACA - 3',
5' - ATT GCG AGA TCT ACG GGG CCT GCT ACT CCA - 3',
5' - ATA GCG GCC GCC CTC GAT TGC GAG AGC TAC - 3',
5' - AAT TCG GGC GGC CGC CAT ACG A - 3',
5' - CTT GAT CTA CCT CCA ATC ATT CAA AGA CTC - 3',
5' - TCT TCA ACT GGG CAG TAA GAA CAA AGC TCA - 3',
5' - AAT TCG CGG CCG CCA TAC GAT TTA GGT GAC ACT ATA GAA T15-3',
5' - TTC GCG GCC GCT ACA GCG GGG GAG ACA T - 3',
5' - AAT TCG CGG CCG CCA TAC GA - 3',
5' - CGA TGA AGG TTG GGG TAA ACA CTC CGG CCT - 3',
5' - GAT CCT GGA ATT CTG ATA AGA CCT TAA GAC TAT TTT AA - 3',
5' - AAT TTG GGA ATT CCA TAA TGA GAC CCT TAA GGT ATT ACT CAG CT
- 3',
5' - GAG TGC TCA AGC TTC AAA ACA AAA TGG CTC ACT TTC TAT CCC
AGA CAA AGC AGA GT - 3',

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5' - GAG TGC TCG ACT CAT TAG GGG GAA ACA TGG TTC CCC CGG GAG
GCG AA - 3',

5' - GAG TGC TCA AGC TTC AAA ACA AAA TGG GGC TCT ACC ACG TCA
CCA ATG ATT GCC CTA AC - 3',

5' - GAG TGC TCG TCG ACT CAT TAA GGG GAC CAG TTC ATC ATC ATA
TCC CAT GCC AT - 3',

5' - GAG TGC AGC TTC AAA ACA AAA TGA GCA CGA ATC CTA AAC CTC
AAA AAA AAA AC - 3',

5' - GAG TGC TCG TCG ACT CAT TAA CCC AAA TTG CGC GAC CTA CGC
CGG GGG TCT GT - 3',

5' - GAG TGC TCA AGC TTA CAA AAC AAA ATG GCA CCA GGC GCC AAG
CAG AAC GTC CAG CTG ATC - 3',

5' - GAG TGC TCC TCG AGG TCG ACT CAT TAC TCG GAC CTG TCC CTA
TCT TCC AGA TCG CAA CG - 3',

5' - GGA TCC GCT AGC GGC GCC AAG CAG AAC GTC CAG CTG ATC AAC
ACC - 3',

5' - GGA TCC AAG CTT TTA CTC GGA CCT GTC CCT ATC TTC CAG ATC
GCA ACG - 3',

5' - CAA TCA TAC CTG ACA G - 3',

5' - GAT AAC CTC TGC CTG A - 3',

5' - GCA TGT CAT GAT GTA T - 3',

5' - ACA ATA CTG GTG TCA C - 3',

5' - CCA GCG GTG GCC TGG TAT TG - 3',

5' - TTT GGG TAA GGT CAT CGA TAC CCT TAC GTG - 3',

5' - ATA TGC GGC CGC CTT CCG TTG GAC TAA - 3',

5' - AAT TCG CGG CCG CCA TAC GAT TTA GGT GAC ACT ATA GAA CCC
CCC CCC CCC CCC - 3',

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5' - CGA CAA GAA AGA CAG A - 3',
5' - CGT TGG CAT AAC TGA T - 3',
5' - CTC TAT GGC AAT GAG G - 3',
5' - AGC TTC GAC GTC ACA T - 3',
5' - CTT GAA TTC GCA ATT TGG GTA AGG TCA TCG ATA CCC TTA CG - 3',
5' - CTT GAA TTC GAT AGA GCA ATT GCA ACC TTG CGT CGT CC - 3',
5' - CTT GAA TTC GGA CGA CGC AAG GTT GCA ATT GCT CTA TC - 3',
5' - CTT GAA TTC CAG CCG GTG TTG AGG CTA TCA TTG CAG TTC - 3',
5' - TGA ACT ATG CAA CAG G - 3',
5' - GGA GTG TGC AGG ATG G - 3',
5' - AAG GTT GCA ATT GCT C - 3',
5' - ACT AAC AGG ACC TTC G - 3',
5' - TAA CGG GTC ACC GCA T - 3',
5' - GTA ATA TGG TGA CAG AGT CA - 3',
5' - GAT CTC TAG AGA AAT CAA TAT GGT GAC AGA GTC A - 3', and
5' - CCC AGC GGC GTA CGC GCT GGA CAC GGA GGT GGC CGC GTC GTG
TGG CGG TGT TGT TCT CGT CGG GTT GAT GGC GC - 3'.

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Here are allowed claims 24 and 26-29 in U.S. Serial No. 08/472,821 (issue fee unpaid):

24. (New) A method for detecting an HCV sequence in a test sample suspected of containing an HCV polynucleotide, wherein the HCV polynucleotide comprises a selected target region, said method comprising:

(a) providing an oligonucleotide capable of selectively and detectably hybridizing to the genome of a hepatitis C virus (HCV) or its complement, wherein the oligonucleotide comprises a contiguous sequence of at least 10 nucleotides complementary to the genome of an HCV or its complement;

(b) incubating the test sample with the oligonucleotide of step (a) under conditions which allow hybrid duplexes to form between the oligonucleotide and the target region specifically relative to other viral agents; and

(c) detecting any hybrids formed between the target region and the oligonucleotide, wherein the presence of said hybrid duplex is indicative of HCV being present in the test sample.

Claim 26. (New) The method of claim 24 wherein the contiguous sequence is at least 12 nucleotides.

Claim 27. (New) The method of claim 24 wherein the contiguous sequence is at least 15 nucleotides.

Claim 28. (New) The method of claim 24 wherein the contiguous sequence is at least 20 nucleotides.

Claim 29. (New) The method of claim 24 wherein the contiguous sequence is present in one of the strands of Figure 1.